



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/775,487

Source:

FFHO

Date Processed by STIC:

12-16-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/775,487

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading!)
 (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or
 scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or
 is Artificial Sequence.
- 11 Use of <220> Sequence(s) missing the <220> "feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/775,487

DATE: 12/16/2004

TIME: 15:24:13

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\12162004\J775487.raw

4 <110> APPLICANT: Faustman, Denise L.
 5 Hayashi, Takuma
 7 <120> TITLE OF INVENTION: Methods For Diagnosing Autoimmune
 8 Disease
 10 <130> FILE REFERENCE: 00786/457003
 12 <140> CURRENT APPLICATION NUMBER: 10/775,487
 13 <141> CURRENT FILING DATE: 2004-02-10
 15 <150> PRIOR APPLICATION NUMBER: 09/258,682
 16 <151> PRIOR FILING DATE: 1999-02-26
 18 <150> PRIOR APPLICATION NUMBER: 09/031,629
 19 <151> PRIOR FILING DATE: 1998-02-27
 21 <160> NUMBER OF SEQ ID NOS: 11
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 32
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Genus/Species
 30 <400> SEQUENCE: 1
 31 gatctaggga ctttcgctg gggactttcc ag
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 40
 35 <212> TYPE: DNA
 36 <213> ORGANISM: genus/species
 38 <400> SEQUENCE: 2
 39 gatctcaggg gaatctccct ctccttttat gggcgtagcg
 41 <210> SEQ ID NO: 3
 42 <211> LENGTH: 10
 43 <212> TYPE: DNA
 44 <213> ORGANISM: genus/species
 46 <400> SEQUENCE: 3
 47 gggactttcc
 49 <210> SEQ ID NO: 4
 50 <211> LENGTH: 10
 51 <212> TYPE: DNA
 52 <213> ORGANISM: genus species
 54 <400> SEQUENCE: 4
 55 gggacgtccc
 57 <210> SEQ ID NO: 5
 58 <211> LENGTH: 10
 59 <212> TYPE: DNA
 60 <213> ORGANISM: genus species
 62 <400> SEQUENCE: 5
 63 ggaaatttcc

Invalid
ResponseInvalid
ResponseSame
errorSame
errorSame
error

(ps.1-2)

Mandatory

32 response
(213) has to
be Artificial40 UNKNOWN OR
a Genus
10 or Speciessee item
10# 10 on
error Summary
Sheet.FYI: which genus/
species?

RAW SEQUENCE LISTING

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Input Set : A:\Seqlist.txt

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65 <210> SEQ ID NO: 6
66 <211> LENGTH: 5
67 <212> TYPE: DNA
68 <213> ORGANISM: genus species
70 <400> SEQUENCE: 6
71 gggac 5
73 <210> SEQ ID NO: 7
74 <211> LENGTH: 5
75 <212> TYPE: DNA
76 <213> ORGANISM: genus species
78 <400> SEQUENCE: 7
79 ggaaa 5
81 <210> SEQ ID NO: 8
82 <211> LENGTH: 5
83 <212> TYPE: DNA
84 <213> ORGANISM: genus species
86 <400> SEQUENCE: 8
87 ctcac
89 <210> SEQ ID NO: 9
90 <211> LENGTH: 5
91 <212> TYPE: DNA
92 <213> ORGANISM: genus species
94 <400> SEQUENCE: 9
95 tttcc 5
97 <210> SEQ ID NO: 10
98 <211> LENGTH: 5
99 <212> TYPE: DNA
100 <213> ORGANISM: genus species
102 <400> SEQUENCE: 10
103 gtccc 5
105 <210> SEQ ID NO: 11
106 <211> LENGTH: 5
107 <212> TYPE: DNA
108 <213> ORGANISM: genus species
110 <400> SEQUENCE: 11
111 tttcc 5

Same errors

Which genus/
Species?

VERIFICATION SUMMARY

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